

## **RAW SEQUENCE LISTING**

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Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,157  
Source: PCT  
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## RAW SEQUENCE LISTING

DATE: 06/22/2005

PATENT APPLICATION: US/10/538,157

TIME: 10:07:45

Input Set : A:\co10227se.APP

Output Set: N:\CRF4\06222005\J538157.raw

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3 <110> APPLICANT: Tobias DASSLER
5 <120> TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF R-ALPHA-LIPOIC ACID BY
6   FERMENTATION
W--> 7 <130> FILE REFERENCE: Co 10227
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/538,157
C--> 10 <141> CURRENT FILING DATE: 2005-06-08
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: PatentIn Ver. 2.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1017
18 <212> TYPE: DNA
19 <213> ORGANISM: Escherichia coli
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(1014)
25 <300> PUBLICATION INFORMATION:
26 <301> AUTHORS: Morris, Timothy W.
27   Reed, Kelynn E.
28   Cronan Jr., John E.
29 <302> TITLE: Identification of the Gene Encoding Lipoate-Protein
30   Ligase A of Escherichia coli
31 <303> JOURNAL: J. Biol. Chem.
32 <304> VOLUME: 269
33 <305> ISSUE: 23
34 <306> PAGES: 16091-16100
35 <307> DATE: 1994
37 <400> SEQUENCE: 1
38 atg tcc aca tta cgc ctg ctc atc tct gac tct tac gac ccg tgg ttt   48
39 Met Ser Thr Leu Arg Leu Leu Ile Ser Asp Ser Tyr Asp Pro Trp Phe
40   1           5           10           15
42 aac ctg gcg gtg gaa gag tgt att ttt cgc caa atg ccc gcc acg cag   96
43 Asn Leu Ala Val Glu Glu Cys Ile Phe Arg Gln Met Pro Ala Thr Gln
44           20           25           30
46 cgc gtt ctg ttt ctc tgg cgc aat gcc gac acg gta gta att ggt cgc   144
47 Arg Val Leu Phe Leu Trp Arg Asn Ala Asp Thr Val Val Ile Gly Arg
48           35           40           45
50 gcg cag aac ccg tgg aaa gag tgt aat acc cgg cgg atg gaa gaa gat   192
51 Ala Gln Asn Pro Trp Lys Glu Cys Asn Thr Arg Arg Met Glu Glu Asp
52           50           55           60
54 aac gtc cgc ctg gcg cgg cgc agt agc ggt ggc ggc gcg gtg ttc cac   240
55 Asn Val Arg Leu Ala Arg Arg Ser Ser Gly Gly Gly Ala Val Phe His
56   65           70           75           80
58 gat ctc ggc aat acc tgc ttt acc ttt atg gct ggc aag ccg gag tac   288

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59 Asp Leu Gly Asn Thr Cys Phe Thr Phe Met Ala Gly Lys Pro Glu Tyr
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62 gat aaa act atc tcc acg tcg att gtg ctc aat gcg ctg aac gcg ctc 336
63 Asp Lys Thr Ile Ser Thr Ser Ile Val Leu Asn Ala Leu Asn Ala Leu
64      100      105      110
66 ggc gtc agc gcc gaa gcg tcc gga cgt aac gat ctg gtg gtg aaa acc 384
67 Gly Val Ser Ala Glu Ala Ser Gly Arg Asn Asp Leu Val Val Lys Thr
68      115      120      125
70 gtc gaa ggc gac cgc aaa gtc tca ggc tcg gcc tat cgc gaa acc aaa 432
71 Val Glu Gly Asp Arg Lys Val Ser Gly Ser Ala Tyr Arg Glu Thr Lys
72      130      135      140
74 gat cgc ggc ttc cac cac ggc acc ttg cta ctc aat gcc gac ctc agc 480
75 Asp Arg Gly Phe His His Gly Thr Leu Leu Leu Asn Ala Asp Leu Ser
76 145      150      155      160
78 cgc ctg gca aac tat ctc aat ccg gat aaa aag aaa ctg gcg gcg aaa 528
79 Arg Leu Ala Asn Tyr Leu Asn Pro Asp Lys Lys Lys Leu Ala Ala Lys
80      165      170      175
82 ggc att acg tcg gta cgt tcc cgc gtg acc aac ctc acc gag ctg ttg 576
83 Gly Ile Thr Ser Val Arg Ser Arg Val Thr Asn Leu Thr Glu Leu Leu
84      180      185      190
86 ccg ggg atc acc cat gag cag gtt tgc gag gcc ata acc gag gcc ttt 624
87 Pro Gly Ile Thr His Glu Gln Val Cys Glu Ala Ile Thr Glu Ala Phe
88      195      200      205
90 ttc gcc cat tat ggc gag cgc gtg gaa gcg gaa atc atc tcc ccg aac 672
91 Phe Ala His Tyr Gly Glu Arg Val Glu Ala Glu Ile Ile Ser Pro Asn
92      210      215      220
94 aaa acg cca gac ttg cca aac ttc gcc gaa acc ttt gcc cgc cag agt 720
95 Lys Thr Pro Asp Leu Pro Asn Phe Ala Glu Thr Phe Ala Arg Gln Ser
96 225      230      235      240
98 agc tgg gaa tgg aac ttc ggt cag gct ccg gca ttc tcg cat ctg ctg 768
99 Ser Trp Glu Trp Asn Phe Gly Gln Ala Pro Ala Phe Ser His Leu Leu
100      245      250      255
102 gat gaa cgc ttt acc tgg ggc ggc gtg gaa ctg cat ttc gac gtt gaa 816
103 Asp Glu Arg Phe Thr Trp Gly Gly Val Glu Leu His Phe Asp Val Glu
104      260      265      270
106 aaa ggc cat atc acc cgc gcc cag gtg ttt acc gac agc ctc aac ccc 864
107 Lys Gly His Ile Thr Arg Ala Gln Val Phe Thr Asp Ser Leu Asn Pro
108      275      280      285
110 gcg ccg ctg gaa gcc ctc gcc gga cga ctg caa ggc tgc ctg tac cgc 912
111 Ala Pro Leu Glu Ala Leu Ala Gly Arg Leu Gln Gly Cys Leu Tyr Arg
112      290      295      300
114 gca gat atg ctg caa cag gag tgc gaa gcg ctg ttg gtt gac ttc ccg 960
115 Ala Asp Met Leu Gln Gln Glu Cys Glu Ala Leu Leu Val Asp Phe Pro
116 305      310      315      320
118 gaa cag gaa aaa gag cta cgg gag tta tcg gca tgg atg gcg ggg gct 1008
119 Glu Gln Glu Lys Glu Leu Arg Glu Leu Ser Ala Trp Met Ala Gly Ala
120      325      330      335
122 gta agg tag 1017
123 Val Arg

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127 <211> LENGTH: 338
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136          20          25          30
138 Arg Val Leu Phe Leu Trp Arg Asn Ala Asp Thr Val Val Ile Gly Arg
139          35          40          45
141 Ala Gln Asn Pro Trp Lys Glu Cys Asn Thr Arg Arg Met Glu Glu Asp
142          50          55          60
144 Asn Val Arg Leu Ala Arg Arg Ser Ser Gly Gly Ala Val Phe His
145   65          70          75          80
147 Asp Leu Gly Asn Thr Cys Phe Thr Phe Met Ala Gly Lys Pro Glu Tyr
148          85          90          95
150 Asp Lys Thr Ile Ser Thr Ser Ile Val Leu Asn Ala Leu Asn Ala Leu
151          100         105         110
153 Gly Val Ser Ala Glu Ala Ser Gly Arg Asn Asp Leu Val Val Lys Thr
154          115         120         125
156 Val Glu Gly Asp Arg Lys Val Ser Gly Ser Ala Tyr Arg Glu Thr Lys
157          130         135         140
159 Asp Arg Gly Phe His His Gly Thr Leu Leu Leu Asn Ala Asp Leu Ser
160   145          150          155          160
162 Arg Leu Ala Asn Tyr Leu Asn Pro Asp Lys Lys Lys Leu Ala Ala Lys
163          165         170         175
165 Gly Ile Thr Ser Val Arg Ser Arg Val Thr Asn Leu Thr Glu Leu Leu
166          180         185         190
168 Pro Gly Ile Thr His Glu Gln Val Cys Glu Ala Ile Thr Glu Ala Phe
169          195         200         205
171 Phe Ala His Tyr Gly Glu Arg Val Glu Ala Glu Ile Ile Ser Pro Asn
172          210         215         220
174 Lys Thr Pro Asp Leu Pro Asn Phe Ala Glu Thr Phe Ala Arg Gln Ser
175   225          230          235          240
177 Ser Trp Glu Trp Asn Phe Gly Gln Ala Pro Ala Phe Ser His Leu Leu
178          245          250          255
180 Asp Glu Arg Phe Thr Trp Gly Gly Val Glu Leu His Phe Asp Val Glu
181          260         265         270
183 Lys Gly His Ile Thr Arg Ala Gln Val Phe Thr Asp Ser Leu Asn Pro
184          275         280         285
186 Ala Pro Leu Glu Ala Leu Ala Gly Arg Leu Gln Gly Cys Leu Tyr Arg
187          290         295         300
189 Ala Asp Met Leu Gln Gln Glu Cys Glu Ala Leu Leu Val Asp Phe Pro
190   305          310          315          320
192 Glu Gln Glu Lys Glu Leu Arg Glu Leu Ser Ala Trp Met Ala Gly Ala
193          325          330          335
195 Val Arg
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Input Set : A:\col0227se.APP

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200 <211> LENGTH: 30  
201 <212> TYPE: DNA  
202 <213> ORGANISM: Artificial Sequence  
204 <220> FEATURE:  
205 <223> OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide  
206 lplA-fwd  
208 <400> SEQUENCE: 3  
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213 <211> LENGTH: 33  
214 <212> TYPE: DNA  
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218 <223> OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide  
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221 <400> SEQUENCE: 4  
222 cgggatccct tatctgaacc gccatttgcg ctg 33

OK

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**VERIFICATION SUMMARY**

DATE: 06/22/2005

PATENT APPLICATION: US/10/538,157

TIME: 10:07:46

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L:7 M:283 W: Missing Blank Line separator, <130> field identifier

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date